II. CLAIMS

1-10. (Cancelled)

11. (Previously Presented) A method of genotyping plants of the species *Triticum aestivum* and the genus *Triticeae* at a microsatellite locus, the method comprising

a) amplifying chromosomal DNA with one or more oligonucleotide primer pairs specifically hybridizing to said locus of a region of said chromosomal DNA, wherein said region of the DNA comprises a repeated ~~dinucleotide~~ motif ~~comprising at least one of the following selected from the group consisting of $(CA:CT)_n$, $(GT:CA)_n$, $(AT:TA)_n$, where n ≥10~~, to obtain an amplification product,

b) wherein each primer pair consists of a first oligonucleotide of SEQ ID NO. x and a second oligonucleotide of SEQ ID NO. *x+1*, and wherein *x*= 1, 3, 5, 7, 9, 11, 13, 15, 17, 19; and

c) size fractionating the amplification product to provide a measure of the said motif of the chromosomal DNA between said primer pairs,

wherein the size of the amplification product is polymorphic for said locus and provides a marker for genotyping said plants.

12. (Previously Presented) The method of claim 11, further comprising the step of using the resulting genotype for a further step chosen from the group consisting of DNA fingerprinting, species identification, relationship studies, similarity studies, characterization of cytological lines, and

genetic mapping.

13. (Cancelled) ~~The method of claim 11, further comprising one or more primer pairs, wherein said primer pairs have a first oligonucleotide of SEQ ID NO: x and a second oligonucleotide of SEQ ID NO: *x+ 1*, and wherein x= 95, 111, 156, 293, 337, 369, 437, 493, 553, and/or 557~~.

14.(New) A method of genotyping plants of the species *Triticum aestivum* and the genus *Triticeae* at a microsatellite locus, the method comprising

d) amplifying chromosomal DNA with one or more oligonucleotide primer pairs specifically hybridizing to said locus of a region of said chromosomal DNA, wherein said region of the DNA comprises a repeated motif, to obtain an amplification product,

e) wherein each primer pair consists of a first oligonucleotide of SEQ ID NO. x and a second oligonucleotide of SEQ ID NO. *x+1*, and wherein *x*= 195, 111, 156, 293, 337, 369, 437; and

f) size fractionating the amplification product to provide a measure of the said motif of the chromosomal DNA between said primer pairs,

wherein the size of the amplification product is polymorphic for said locus and provides a marker for genotyping said plants.

15. (New) The method of claim 14, further comprising the step of using the resulting genotype for a further step chosen from the group consisting of DNA

fingerprinting, species identification, relationship studies, similarity studies, characterization of cytological lines, and genetic mapping.